

Table S3. List of alternatively expressed probe sets.

Affymetrix probe set	Gene symbol	Entrez gene ID	Factor (RMA) ¹	Factor (Iter-PLIER) ²	splicing event	Predicted outcome
3730694	<i>ace</i>	1636	2.68	3.84	APA ³	NMD ⁴
2394641	<i>acot7</i>	11332	2.16	3.29	cassette exon	NMD
3927468	<i>adams1</i>	9510	2.53	3.63	internal probe set in first exon	
3700223	<i>adams18</i>	170692	2.08	2.27	internal probe set in first exon	
3554361	<i>adssl1</i>	122622	0.23	0.16	first probe set	
2532841	<i>atg1611</i>	55054	2.22	2.22	internal probe set in last exon	
4005893	<i>cask</i>	8573	0.43	0.32	cassette exon	alt. protein
2473995	<i>cenpa</i>	1058	2.10	4.00	first probe set	
3372287	<i>cugbp1</i>	10658	0.42	0.34	APS ⁵	alt. N-terminus
3125254	<i>dlc1</i>	10395	0.49	0.38	constitutive exon	alt. Protein
3125257	<i>dlc1</i>	10395	0.49	0.41	constitutive exon (one of two probe sets)	alt. protein
3850153	<i>dnmt1</i>	1786	2.46	2.50	first probe set	
3403018	<i>eno2</i>	2026	0.36	0.26	constitutive exon	no AUG ⁶
3403020	<i>eno2</i>	2026	0.46	0.36	cassette exon	NMD
2610263	<i>fancd2</i>	2177	0.28	0.41	constitutive exon	NMD
2367115	<i>fmo4</i>	2329	0.44	0.28	internal probe set in last exon	
2732693	<i>fras1</i>	80144	0.49	0.34	constitutive exon (one of two probe sets)	NMD
3484601	<i>fry</i>	10129	2.50	2.73	constitutive exon	alt. protein
3484607	<i>fry</i>	10129	2.10	2.23	constitutive exon	alt. protein
2946384	<i>hist1h4h</i>	8365	2.27	2.14	APS (first probe set)	alt. 5'UTR
3848349	<i>insr</i>	3643	0.45	0.44	constitutive exon	no AUG
3918909	<i>itsn1</i>	6453	2.31	3.12	APA	alt. C-terminus
3980611	<i>kif4a</i>	24137	3.51	4.89	internal probe set in last exon	
3631510	<i>larp6</i>	55323	0.40	0.33	APA	alt. C-terminus
3631511	<i>larp6</i>	55323	0.33	0.28	APA	alt. C-terminus
2575045	<i>lims2</i>	55679	0.49	0.24	APS (first probe set)	alt. N-terminus
2669251	<i>lrrkip2</i>	9209	0.39	0.34	cassette exon	alt. protein
3568681	<i>max</i>	4149	2.30	3.05	intron retention	alt. C-terminus
3568682	<i>max</i>	4149	3.63	4.50	intron retention	alt. C-terminus
3568683	<i>max</i>	4149	2.66	3.48	intron retention	alt. C-terminus
3568684	<i>max</i>	4149	3.32	4.38	intron retention	alt. C-terminus

3568685	<i>max</i>	4149	2.68	3.43	intron retention	alt. C-terminus
3568686	<i>max</i>	4149	2.66	3.32	intron retention	alt. C-terminus
3235792	<i>mcm10</i>	55388	0.28	0.46	constitutive exon	no AUG
2648678	<i>mme</i>	4311	0.47	0.41	APS (first probe set)	alt. 5'UTR
2752752	<i>neil3</i>	55247	2.28	3.16	constitutive exon (one of two probe sets)	alt. C-terminus
3031738	<i>nos3</i>	4846	2.01	2.79	constitutive exon	NMD
3092890	<i>nrg1</i>	3084	0.40	0.43	APS (one of three probe sets)	alt. N-terminus
2751119	<i>palld</i>	23022	0.50	0.37	constitutive exon	alt. protein
3381233	<i>pde2a</i>	5138	0.48	0.40	first probe set	
3811162	<i>pign</i>	23556	0.34	0.39	cassette exon	alt. 5'UTR
3908935	<i>ptgis</i>	5740	0.30	0.26	last probe set	
3196920	<i>rfx3</i>	5991	0.27	0.19	cassette exon	alt. 5'UTR
2683902	<i>robo1</i>	6091	0.23	0.25	APS	alt. N-terminus
3108191	<i>sdc2</i>	6383	0.46	0.35	last probe set	
2409153	<i>slc2a1</i>	6513	0.26	0.21	first probe set	
3373876	<i>slc43a3</i>	29015	0.49	0.41	APS (first probe set)	alt. 5'UTR
2699159	<i>slc9a9</i>	285195	2.41	4.56	last probe set	
4021157	<i>smarca1</i>	6594	0.50	0.41	last probe set	
3190593	<i>sptan1</i>	6709	0.44	0.40	cassette exon	alt. protein
2581434	<i>stam2</i>	10254	0.29	0.35	internal probe set in last exon	
2411269	<i>stil</i>	6491	2.68	2.89	cassette exon or APS (first probe set)	alt. 5'UTR
3908437	<i>sulf2</i>	55959	2.48	2.53	first probe set	
3094806	<i>tacc1</i>	6867	0.31	0.37	cassette exon	alt. 5'UTR
3776512	<i>tgif1</i>	7050	0.43	0.30	internal probe set in first exon	
3597364	<i>tpm1</i>	7168	0.41	0.31	APS (one of two probe sets)	alt. N-terminus
3576846	<i>trip11</i>	9321	5.82	3.12	cassette exon (one of two probe sets)	alt. protein
3381833	<i>ucp2</i>	7351	2.11	2.62	first probe set	
2908181	<i>vegfa</i>	7422	0.45	0.40	internal probe set in first exon	
3435119	<i>wdr66</i>	144406	0.38	0.30	constitutive exon	NMD
3290223	<i>zwint</i>	11130	2.75	4.35	intron retention	alt. 3'UTR

¹ Fold change as predicted by RMA.

² Fold change as predicted by Iter-PLIER.

³ APA = alternative polyadenylation

⁴ NMD = nonsense mediated decay

⁵ APS = alternative promoter selection

⁶ no AUG = the constitutive exon is the first exon of the open reading frame